

Robinson



1600

## RAW SEQUENCE LISTING

DATE: 02/11/2003

PATENT APPLICATION: US/09/659,379

TIME: 20:10:26

Input Set : N:\Crf3\RULE60\09659379.txt

Output Set: N:\CRF4\02112003\I659379.raw

## SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Vinik, Aaron

6 Pittenger, Gary

7 Rafaeloff-Phail, Ronit

8 Barlow, Scott

10 (ii) TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF

11 INGAP IN BACTERIAL AND EUKARYOTIC CELLS

13 (iii) NUMBER OF SEQUENCES: 6

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Banner & Witcoff, Ltd.

17 (B) STREET: 1001 G Street, N.W.

18 (C) CITY: Washington

19 (D) STATE: DC

20 (E) COUNTRY: USA

21 (F) ZIP: 20001

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Diskette

25 (B) COMPUTER: IBM Compatible

26 (C) OPERATING SYSTEM: DOS

27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/659,379

C--> 31 (B) FILING DATE: 08-Sep-2000

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

W--> 35 (A) APPLICATION NUMBER: US/08/909,725

36 (B) FILING DATE: 12-AUG-1997

W--> 37 (A) APPLICATION NUMBER: 08/741,096

38 (B) FILING DATE: 30-OCT-1996

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Kagan, Sarah A

44 (B) REGISTRATION NUMBER: 32,145

45 (C) REFERENCE/DOCKET NUMBER: 0570.05173

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 202-508-9100

49 (B) TELEFAX: 202-508-9299

50 (C) TELEX: 97430 BMB UT

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 94 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: single

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59          (D) TOPOLOGY: linear
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64      CTGCAAGACA GGTACCATGA TGCTTCCCAT GACCCTCTGT AGGATGTCTT GGATGCTGCT      60
65      TTCCTGCCTG ATGTTCTTTT CTTGGGTGGA AGGT      94
67      (2) INFORMATION FOR SEQ ID NO: 2:
69          (i) SEQUENCE CHARACTERISTICS:
70              (A) LENGTH: 31 base pairs
71              (B) TYPE: nucleic acid
72              (C) STRANDEDNESS: single
73              (D) TOPOLOGY: linear
76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
78      CCGCGGATCC CGAAGAATCT CAAAAGAAAC T      31
80      (2) INFORMATION FOR SEQ ID NO: 3:
82          (i) SEQUENCE CHARACTERISTICS:
83              (A) LENGTH: 32 base pairs
84              (B) TYPE: nucleic acid
85              (C) STRANDEDNESS: single
86              (D) TOPOLOGY: linear
89      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
91      GACCGGCTCG AGTGCTCTTC CTGAGTGAAT CC      32
93      (2) INFORMATION FOR SEQ ID NO: 4:
95          (i) SEQUENCE CHARACTERISTICS:
96              (A) LENGTH: 558 base pairs
97              (B) TYPE: nucleic acid
98              (C) STRANDEDNESS: single
99              (D) TOPOLOGY: linear
101         (ii) MOLECULE TYPE: cDNA
103         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
105         CCGCGGATCC CGAAGAATCT CAAAAGAAAC TGCCTTCTTC ACGTATAACC TGTCCTCAAG      60
106         GCTCTGTAGC CTATGGGTCC TATTGCTATT CACTGATTTT GATACCACAG ACCTGGTCTA      120
107         ATGCAGAACT ATCCTGCCAG ATGCATTTCT CAGGACACCT GGCATTTCTT CTCAGTACTG      180
108         GTGAAATTAC CTTCTGTGCC TCCCTTGTTGA AGAACAGTTT GACGGCCTAC CAGTACATCT      240
109         GGATTGGACT CCATGATCCC TCACATGGTA CACTACCCAA CGGAAGTGGA TGGAAGTGGA      300
110         GCAGTTCCAA TGTGCTGACC TTCTATAACT GGGAGAGGAA CCCCTCTATT GCTGCTGACC      360
111         GTGGTTATTG TGCAGTTTTG TCTCAGAAAT CAGGTTTTCA GAAGTGGAGA GATTTTAAAT      420
112         GTGAAAATGA GCTTCCCTAT ATCTGCAAAT TCAAGGTCTA GGGCAGTTCT AATTTCAACA      480
113         GCTTGAAAAT ATTATGAAGC TCACATGGAC AAGGAAGCAA GTATGAGGAT TCACTCAGGA      540
114         AGAGCACTCG AGCCGGTC      558
116      (2) INFORMATION FOR SEQ ID NO: 5:
118          (i) SEQUENCE CHARACTERISTICS:
119              (A) LENGTH: 26 amino acids
120              (B) TYPE: amino acid
121              (C) STRANDEDNESS: single
122              (D) TOPOLOGY: linear
124          (ii) MOLECULE TYPE: peptide
126          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
128      Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
129      1          5          10          15
130      Cys Leu Met Phe Leu Ser Trp Val Glu Gly

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131          20          25
133 (2) INFORMATION FOR SEQ ID NO: 6:
135     (i) SEQUENCE CHARACTERISTICS:
136         (A) LENGTH: 175 amino acids
137         (B) TYPE: amino acid
138         (C) STRANDEDNESS: single
139         (D) TOPOLOGY: linear
141     (ii) MOLECULE TYPE: protein
143     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
145 Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
146  1          5          10          15
147 Cys Leu Met Phe Leu Ser Trp Val Glu Gly Glu Glu Ser Gln Lys Lys
148          20          25          30
149 Leu Pro Ser Ser Arg Ile Thr Cys Pro Gln Gly Ser Val Ala Tyr Gly
150          35          40          45
151 Ser Tyr Cys Tyr Ser Leu Ile Leu Ile Pro Gln Thr Trp Ser Asn Ala
152          50          55          60
153 Glu Leu Ser Cys Gln Met His Phe Ser Gly His Leu Ala Phe Leu Leu
154          65          70          75          80
155 Ser Thr Gly Glu Ile Thr Phe Val Ser Ser Leu Val Lys Asn Ser Leu
156          85          90          95
157 Thr Ala Tyr Gln Tyr Ile Trp Ile Gly Leu His Asp Pro Ser His Gly
158          100         105         110
159 Thr Leu Pro Asn Gly Ser Gly Trp Lys Trp Ser Ser Ser Asn Val Leu
160          115         120         125
161 Thr Phe Tyr Asn Trp Glu Arg Asn Pro Ser Ile Ala Ala Asp Arg Gly
162          130         135         140
163 Tyr Cys Ala Val Leu Ser Gln Lys Ser Gly Phe Gln Lys Trp Arg Asp
164          145         150         155         160
165 Phe Asn Cys Glu Asn Glu Leu Pro Tyr Ile Cys Lys Phe Lys Val
166          165         170         175

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## VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:37 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)